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Trend of HIV infection among pediatric tuberculosis patients in Tanzania, 2006- 2010

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Background: HIV testing among tuberculosis (TB) patients is critical in improving morbidity and mortality, as those found to be HIV positive will be offered a continuum of care including ART, if indicated.In Tanzania, the TB/HIV collaborative activities started in 2006, however, the complex interaction between the dual HIV and TB in children in Tanzania is still underreported.

We conducted this study with the aim to determine prevalence of TB/HIV co-infection in children; trend of HIV testing among children with TB; and association of HIV and TB infections in children.

Methods & Materials: We conducted a retrospective review of data involving children below 15 years enrolled in the TB clinics between 2006 and 2010 in selected four regions in Tanzania. All children on TB treatment were eligible.

Results: A total of 4,684 TB confirmed children were reviewed with the mean age of 6.2± 4.2 years. Almost half 2284 (48.4%) of them were tested for HIV. The prevalence of HIV among the TB confirmed children was 905 (39.6%). The prevalence of HIV increased from 230 (22%) in 2006 to 270 (44%) in 2009 then dropped to 255 (37%) in 2010 and the changes were significant (p<0.05). The proportion of children tested for HIV among TB patients increased significantly from 104 (25%) in 2006 to 671 (93%) in 2010 (p=0.001). The <5 years had lower risk of HIV infection [Odds ratio (OR) = 0.8; 95% Confidence Interval (CI): 0.7 – 1.0]. HIV positive children had higher risk of developing EPTB [OR=1.4; 95% CI: 1.2-1.7]. HIV positivity was statistically associated with TB treatment failure [OR= 1.4, 95%CI: 1.0-2.0], TB relapse [OR= 2.5, 95%CI: 1.5-4.3] as well as increased risk of death rate among TB pediatric children [OR= 2.1, 95%CI: 1.4-3.1]

Conclusion: There has been a significant increase in HIV testing rate with years as well as increased prevalence of HIV among TB children. HIV infection among TB patients is associated with EPTB, treatment failure and increased death rates. HIV testing among TB patients will facilitate early initiation of HIV care and treatment services thus reduce the above associated risks.

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High prevalence of minor HIV drug resistant strains in a treatment naive population in Kenya

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Background: The advent of antiretroviral treatment (ART) has resulted in dramatic reduction in AIDS related morbidity and mortality. However the emergence and spread of antiretroviral drug resistance (DR) threatens to negatively impact on treatment regimens and compromise efforts to control the epidemic. It is recommended that surveillance of drug resistance occur in conjunction with scale-up efforts to ensure appropriate first-line therapy is offered relative to the resistance that exists. However standard resistance testing methods used in Subsahara Africa rely on techniques that miss out on low abundance DR variants (LADRVs) which have been documented to contribute to treatment failure. The use of next generation sequencing (NGS) has been shown to be more sensitive for LADRVS. We have carried out a preliminary investigation using NGS to determine the prevalence of LDRVS among a drug naïve population in North Rift Kenya.

Methods & Materials: Antiretroviral naïve patients attending a care clinic at Moi Teaching and Referral Hospital (MTRH) in Eldoret, Kenya were requested and with consent provided blood samples for DR analysis. DNA was extracted, amplified and nested PCR conducted on pol RT region using with primers tagged with multiplex identifiers (MID). Resulting PCR amplicons were purified, quantified and pyrosequenced using a GS FLX Titanium PicoTiterPlate (Roche). Valid pyrosequencing reads were aligned with HXB-2 and the frequency and distribution of nucleotide and amino acid changes determined using an in-house Perl script. DR mutations were identified using the IAS-USA HIV DR mutation database.

Results: Sixty samples were successfully sequence of which 25 were subtype A, 11 subtype D, 1 Subtype C and the remaining were recombinants. Forty six (76.6%) had at least one drug resistance mutation; with 25 (41.6%) indicated as major and the rest 21 (35%) indicated as minor. The most prevalent mutation was NRTI position K219Q/R (11 of 46, 24%) followed by NRTI M184 V (5 of 46, 11%) and NNRTI K103N (4 of 46,9%).

Conclusion: Our use of NGS technology revealed a high prevalence of LADRVs among drug naive populations in Kenya. The impact of these mutations on clinical outcome on ART can only be ascertain through a long term follow-up.

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